

Amendments to the Drawings:

Please add the following new drawings, Figures 11, 12, 13, 14, 15, 16, 17, 18 and 19, after Figure 10. The attached new sheets of drawings includes Figures 11, 12, 13, 14, 15, 16, 17, 18 and 19 to be added.

Attachment: New Sheets

(3) Sequence Description: Figure 11

1	ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCC	
5	MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro	16
49	ACTCGACTTCTTTTGAATATCTTGAAGAAAAATATGAAGAGCATTTG	
	ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu	32
10	97 TATGAGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTG	
	TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu	48
145	GGTTTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAA	
	GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys	64
15	193 TTAACACAGTCTATGGCCATCATACTTATATAGCTGACAAGCACAAC	
	LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn	80
241	ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAA	
20	MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu	96
289	GGAGCGGTTTTGGATATTAGATACGGTGTTCGAGAATTGCATATAGT	
	GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer	112
337	AAAGACTTTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAA	
25	LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu	128
385	ATGCTGAAAATGTTCTGAAGATCGTTTATGTCATAAAACATATTTAAAT	
	MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn	144
433	GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGAT	
30	GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp	160
481	GTTGTTTTATACATGGACCCAATGTGCCTGGATGCGTTCCCAAAATTA	
35	ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu	176

	529	GTTTGTTTTAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC	
		ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr	192
	577	TTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCC	
5		LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla	208
	625	ACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGTTCCGCGT	
		ThrPheGlyGlyGlyAspHisProProLysSerAspLeuValProArg	224
10	673	GGATCCATGAGCACGATTCCCAAACCTCAAAGAAAAACCAAACGTAAC	
		GlySerMetSerThrIleProLysProGlnArgLysThrLysArgAsn	240
	721	ACCAACCGTCGCCCCACAGGAATTCATCGTGACTGACTGA	
		ThrAsnArgArgProGlnGluPheIleValThrAspEnd	252
15			
		(4) <u>Sequence Description</u> : Figure 12	
	1	ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCC	
		MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro	16
20	49	ACTCGACTTCTTTTGAATATCTTGAAGAAAAATATGAAGAGCATTTG	
		ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu	32
	97	TATGAGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTG	
		TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu	48
25			
	145	GGTTTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAA	
		GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys	64
	193	TTAACACAGTCTATGGCCATCATACTTATATAGCTGACAAGCACAAAC	
30		LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn	80
	241	ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAA	
		MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu	96
35	289	GGAGCGGTTTTGGATATTAGATACGGTGTTCGAGAATTGCATATAGT	
		GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer	112

	337	AAAGACTTTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAA	
		LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu	128
5	385	ATGCTGAAAATGTTCTGAAGATCGTTTATGTCATAAAACATATTTAAAT	
		MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn	144
	433	GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGAT	
		GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp	160
10	481	GTTGTTTTTATACATGGACCCAATGTGCCTGGATGCGTTCCCAAATTA	
		ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu	176
	529	GTTTGTTTTTAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC	
15		ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr	192
	577	TTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCC	
		LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla	208
20	625	ACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGTTCCGCGT	
		ThrPheGlyGlyGlyAspHisProProLysSerAspLeuValProArg	224
	673	GGATCCGACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTT	
		GlySerAspValLysPheProGlyGlyGlyGlnIleValGlyGlyVal	240
25	721	TACTTGTTGCCGCGCAGGGAATTCATCGTGACTGACTGA	
		TyrLeuLeuProArgArgGluPheIleValThrAspEnd	252

5

(6) Sequence Description: Figure 13

1	ATGTCCCCTATACTAGGTTATTGAAAATTAAGGGCCTTGTGCAACCC	
	MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro	16
10	49 ACTCGACTTCTTTTGAATATCTTGAAGAAAAATATGAAGAGCATTTG	
	ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu	32
	97 TATGAGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTG	
	TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu	48
15	145 GGT TTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAA	
	GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys	64
	193 TTAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAAAC	
20	LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn	80
	241 ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAA	
	MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu	96
25	289 GGAGCGGTTTTGGATATTAGATACGGTGTTCGAGAATTGCATATAGT	
	GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer	112
	337 AAAGACTTTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAA	
	LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu	128
30	385 ATGCTGAAAATGTTCGAAGATCGTTTATGTCATAAAACATATTTAAAT	
	MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn	144
	433 GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGAT	
35	GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp	160

481 GTTGTTTTATACATGGACCCAATGTGCCTGGATGCGTTCCCAAATTA  
ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu 176

5 529 GTTTGTTTTAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC  
ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr 192

577 TTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCC  
LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla 208

10 625 ACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGTTCCGCGT  
ThrPheGlyGlyGlyAspHisProProLysSerAspLeuValProArg 224

673 GGATCCAGCACGATTCCCAAACCTCAAAGAAAAACCAAACGTAACACC  
GlySerSerThrIleProLysProGlnArgLysThrLysArgAsnThr 240

15 721 AACCGTCGCCCACAGGACGTCAAGTTCCCGGGTGGCGGTCAGATCGTT  
AsnArgArgProGlnAspValLysPheProGlyGlyGlyGlnIleVal 256

769 GGTGGAGTTTACTTGTGCGCGCAGGGAATTCATCGTGACTGACTGA  
20 GlyGlyValTyrLeuLeuProArgArgGluPheIleValThrAspEnd 271

(7) Sequence Description: Figure 14

5'-GATCCATGAGCACGATTCCCAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGC  
CCACAGG-3'

25 (8) Sequence Description: Figure 15

5'-AATTCCTGTGGGCGACGGTTGGTGTTACGTTTGGTTTTCTTTGAGGTTTGGGAATCGT  
GTCATG-3'

(9) Sequence Description: Figure 16

30 5'-GATCCGACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTGCGG  
CGCAGG-3'

(10) Sequence Description: Figure 17

5'-AATTCCTGCGCGGCAACAAGTAACTCCACCAACGATCTGACCGCCACCCGGGAACTT  
GACGTCG-3'

5 (13) Sequence Description: Figure 18  
5'-GAATTCTTACCTGCGCGGCAACAAGTAAACTC-3'

(14) Sequence Description: Figure 19  
5'-GCTGGATCCAGCACGATTCCCAAACCTCAAAG-3'